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1/6

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Figure 1a

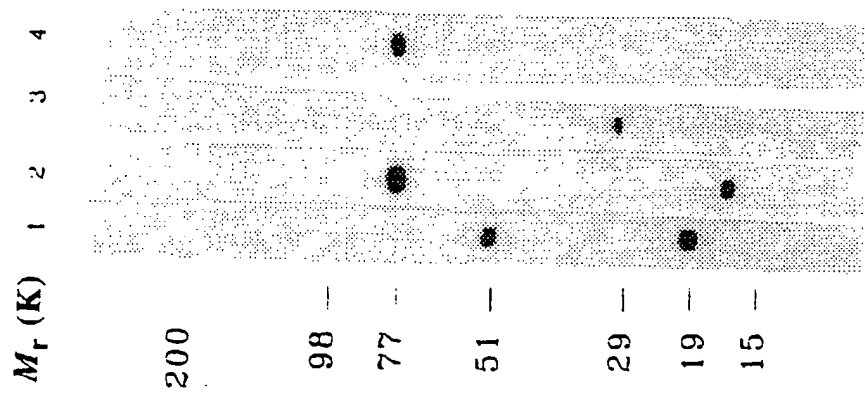
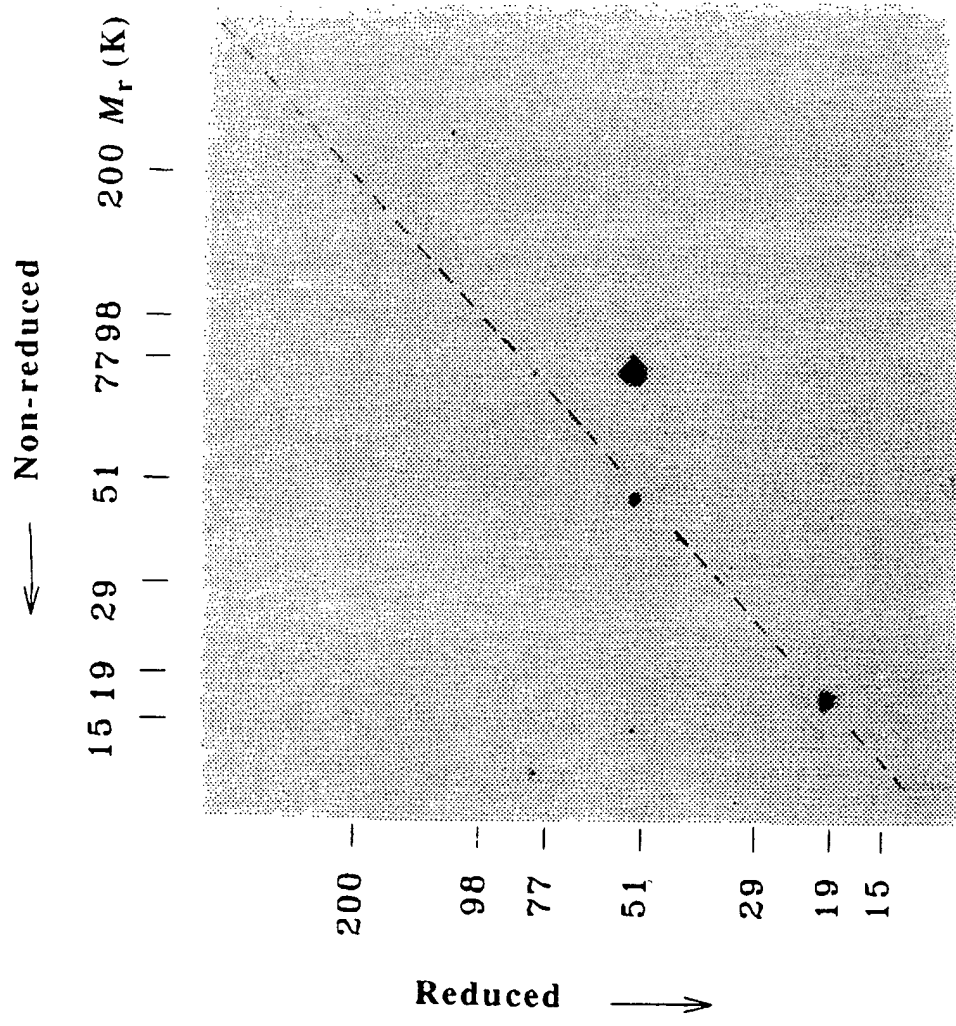


Figure 1b



2/6

Figure 2

— C1r/C1s —>		
MASP-2	TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYRLRLYFTHFDLELSHLCEYDFVKLSSGAKVLATLGGQESTDTERAPGKDT	90
MASP-1	HTVELNNMFGQIQSPGYPDSYPSDSEVTWNITVPDGFRIKLYFMHFNLESSYLCEYDYVKVETEDQVLATFGRETDTDEQTPGQEV	87
C1r	SIIPIQKLFGEVTSPLFPKPYPNFETTTVITVPTGYRVKLVFQQFDLEPSEGGFYDYVKISADKKSLGRPGQLGSLGNPPGKKE	87
C1s	EPTMYGEILSPNYPQAYPSEVEKSWDIEVPEGYGIHLFYTHLDIELSENCAYDSVQIIISGDTEEGRLGGQRSSNNPHSPIVEE	83
* * * * *		
EGF —>		
MASP-2	FYSLGSSLDITFRSDYSNEKP FTGFEAFYAAEDIDEQ VAPGEA PTCDDHCHNHLGGFYSCRAGYVLHRNKRTCSALCS	170
MASP-1	VLSPGSFMSITFRSDFSNEER FTGFDAYMAVDVDECK EREDEE LSCDHYCHNYIGGYYSCSRFGYILHTDNRTERVECS	167
C1r	FMSQGNKMLLTFTHTDFSNEENGTFMYKGFLLAYQAVALDECSRSKSGEEDPQPOQHLCHNYVGGYFSCSRPGYELQEDRHSQAECS	177
C1s	FQVPYNKLQVIFKSDFSNEER FTGFAAYVATDINECT DFVD VPQSHFCHNNFIGGYFSCSPPPEYFLHDDMKNGGVNCS	161
* * * * *		
— C1r/C1s —>		
MASP-2	GQVFTQSGELSSPEYPRPYPKLSSCTYSISLEEGFSVILDFV ESPDVET HPETLCOPYDFLKIQTDRREEHGGPFGKTLPHR IETKS	256
MASP-1	DNLFTQRTGVTSPDFPNPYPKSSEKLYTIELEEGFMVNLOFE DIFDIED HPEVPCPYDYIKIKVGPVKLPFGGKAPPEP ISTQS	253
C1r	SELYTEASGYISSLEYPRSYPPDLRCNYSIRVERGLTLHLKFL BPFDDDD HQQVHCOPYDQLQIYANGKNIGEFQKQRPDP LDTSS	263
C1s	GDVFTALIGEIASPNYPKPYPENSRCYQIRLEKGFQVVVTLRREDFDVEAADSAGNC LDSLVFVAGDRQFGPYCGHGFPGPLNIETKS	250
* * * * *		
CCP-1 —>		
MASP-2	NTVTITFTVDES GDHTGKWIHYTSTAQPCPYPMAPPN GHVSPVQAKYILKDSFSIFCETGYELLQGHLPKLSFTAVQCKDGSWDRPMPA	345
MASP-1	HSVLILFHSNDNGENRGWRLSYRAAGNECPQLQPPVH GKIEPSQAKYFFKDQVLVSCDTGYKVLKDNVEMDTFQIECLDKGTWSNKIPT	342
C1r	NAVDLLFFTDGSDSRGWKLRYTTEIIKEPQPKTLDEFTIIQNLPQYQFRDYFIATCKQGYQLIEGNQVLHSFTAVQDDGTWHRAMPR	353
C1s	NALDIIFQTDLTGQKKGWKLRYHGDPMPCPKEDTPN SVWEPAKAKYVFRDVVQITCLDGFVEVGRVGATSFYSTCQSNKGWSNSKLK	338
* * * * *		
CCP-2 —>		
MASP-2	ESIVDEGPPDDLPSGRVEYITGPGVTITYKAVIQYSCETFTYM K VNDGKYVCEADGEFTSSKGEKSLPVCEPVGGLS ARTT	426
MASP-1	EKIVDGRAPGELEHGLITFSTRNNLTYYKSEIKYSCQEPYKML NNNTGIYTCQAQGVMMNKVLGRSLPTCLPVGGLPKFSRKL	426
C1r	EKIKDGGQPRNLPNGDFRYTTTGMVNTYKARIQYCHEPYKMQTRAGSRESEQGVYTCTAQGIWKNEQKGEKIPRELFPVGKPVNPFVEQ	443
C1s	QOPVDGIPESIEENGKVE DPESTLFGSVIRYTCPEPYMYE NGGGGEYHCAGNGSWVNEVLGPPELPKCPVPGVPREPFEFEE	419
* * * * *		
serine protease —>		
MASP-2	GGRIYGGQKAKPGDFPQVLLGGTTA AGALLYDNWVLTAAH AVYEQKHDASALDIRMGTLLKRLSPHYTQAWSEAVFIHEG	507
MASP-1	MARIFNGRPAQKGTTPWIAMLSHLNQPFQGGSLGSSWIVTAAHCLHQSLLDPKDPPTLRSDLLSPSD FKIIIGKHWRLSRSDENEQHLG	515
C1r	RQRIIGGQKAKMGNFPPWQVFTNIHGRG GGALLGDRWILTAAH TLYPKEHEAQSNASLDVFLGHTNVEELMKLGNHP IRRV	523
C1s	KQRIIGGSDADIKNFPPWQVFDNPWA GGALINEYVWLTAAH VVEGNREPTMYVGSTSVQTSRLAKSKMLT PEHVFIHPG	498
* * * * *		
FDNDIALIKLNKVVINSNITPICLPKAEASFMRITDDIGTASGWGLTQRGFLARNLMYVDIPVDHQKATAAYEK		589
MASP-2	YTHDAG	
MASP-1	VKHTTLHPKYDPNTFENDVALVELLESFVLNAPVMPICLP EGPOQEGAMVIVSGWQKQFLQRPETLMIEIPIVDHSTOKAY	599
C1r	SVHPDYRQDESYN FEGDIALLELENSVTLGPNLLPICLP DNDTFYDLGLMGYVSGFGVMEEK IAHDLRFVRLPVANPQACEN WLR	608
C1s	WKLEEV PEGRTN FDNDIALVRLKDPVKMGPTVSPICLPPTSSDYNLMDGLGLISGWGRTEKRDRAVRLKAARLPVAPLRKEKEVKVE	586
* * * * *		
PPYPRG SVTANMLCAGLES GGKDSRGDSGGALVFLDS ETERWFVGGIVSWGSMNCGEAGQYGVYTKVINIYIPWIENIISDF		671
MASP-2		
MASP-1	APLKK KVTRDMICAGEKEGGKDAESGDSGGPMVTLNR ERGQWYLVGTVSWGD DCGKKDRYGVYSYIHHNKDWIQRVTGVRN	680
C1r	GKNRMD VFSQNMFCAGHPSLKQDAEGDSGGVFAVRDP NTDRAWATGIVSWG I GQSRG YGFYTKVLNVYDWMIKKEMEED	688
C1s	KPTADAEAYVFTPNMICAGGEK GMDSCKGDSGGAFVQDPNDKTKFYAAGLVSWGP QCGT YGLYTRVKNVYDWMIKMTQENSTPRED	673
* * * * *		

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3/6 Figure 3a

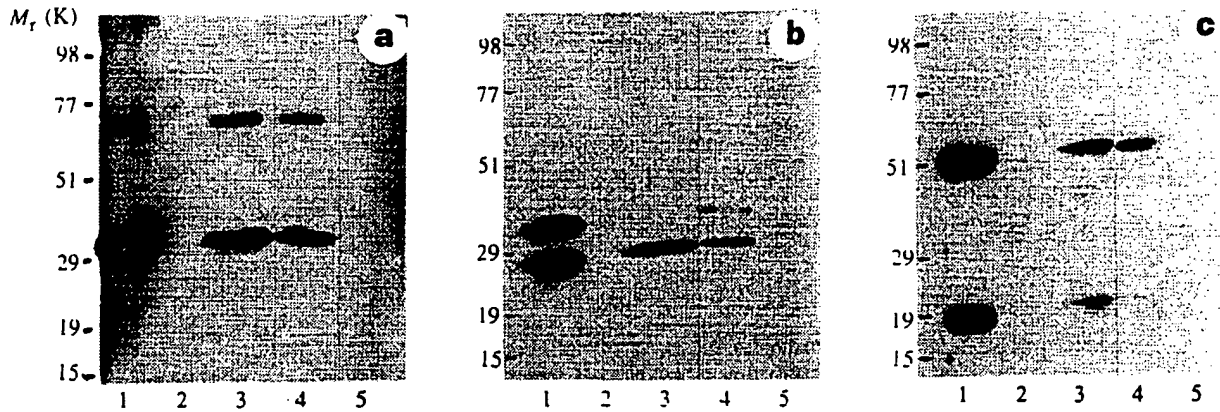
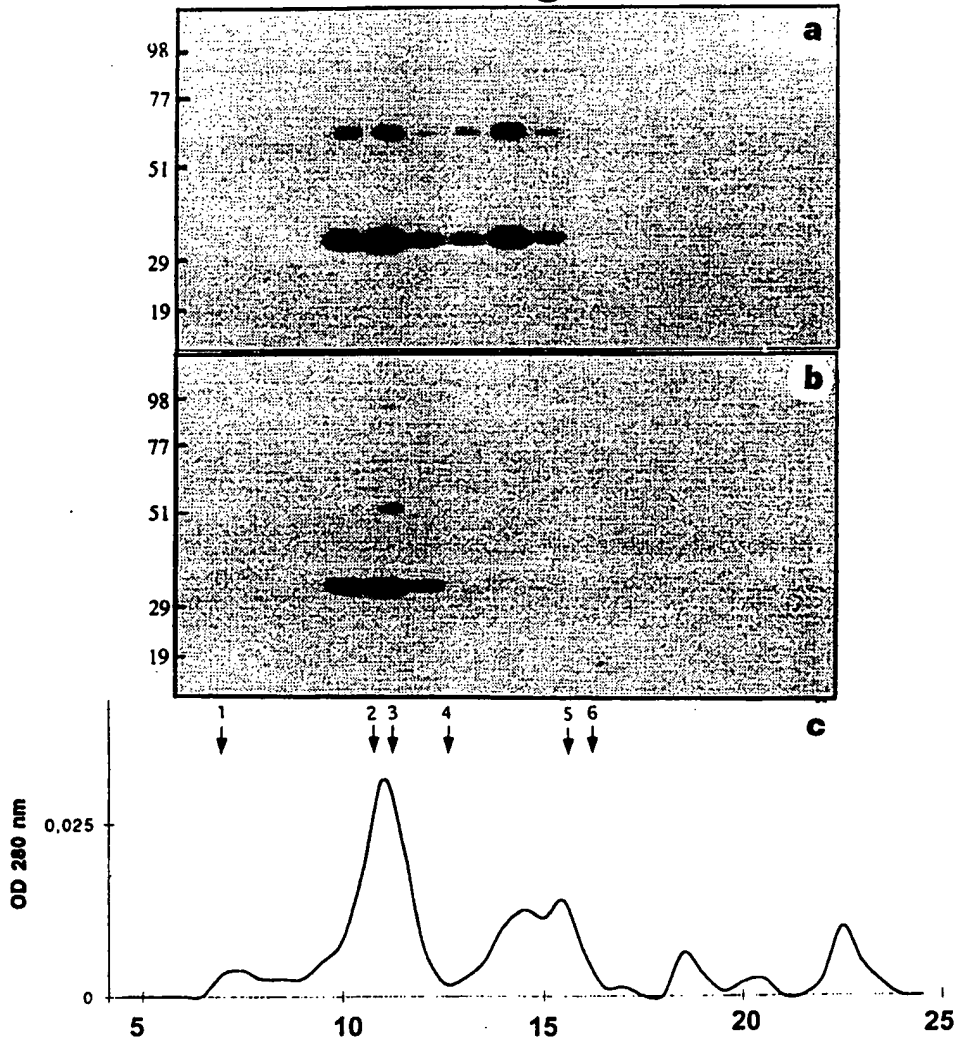


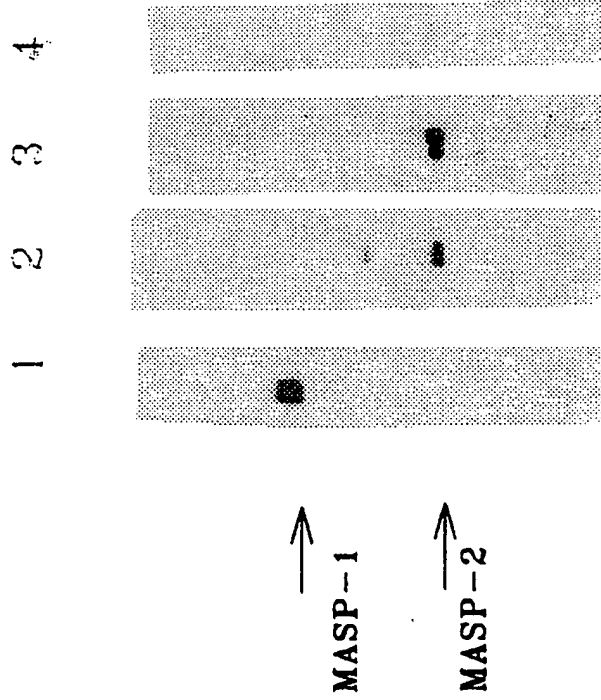
Figure 3b



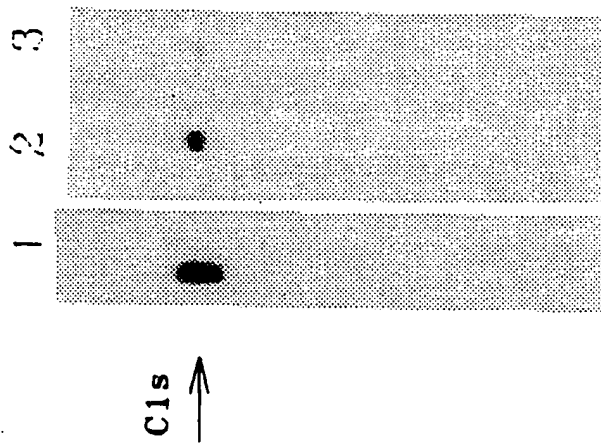
4/6

Figure 4

Blot of MBL preparation

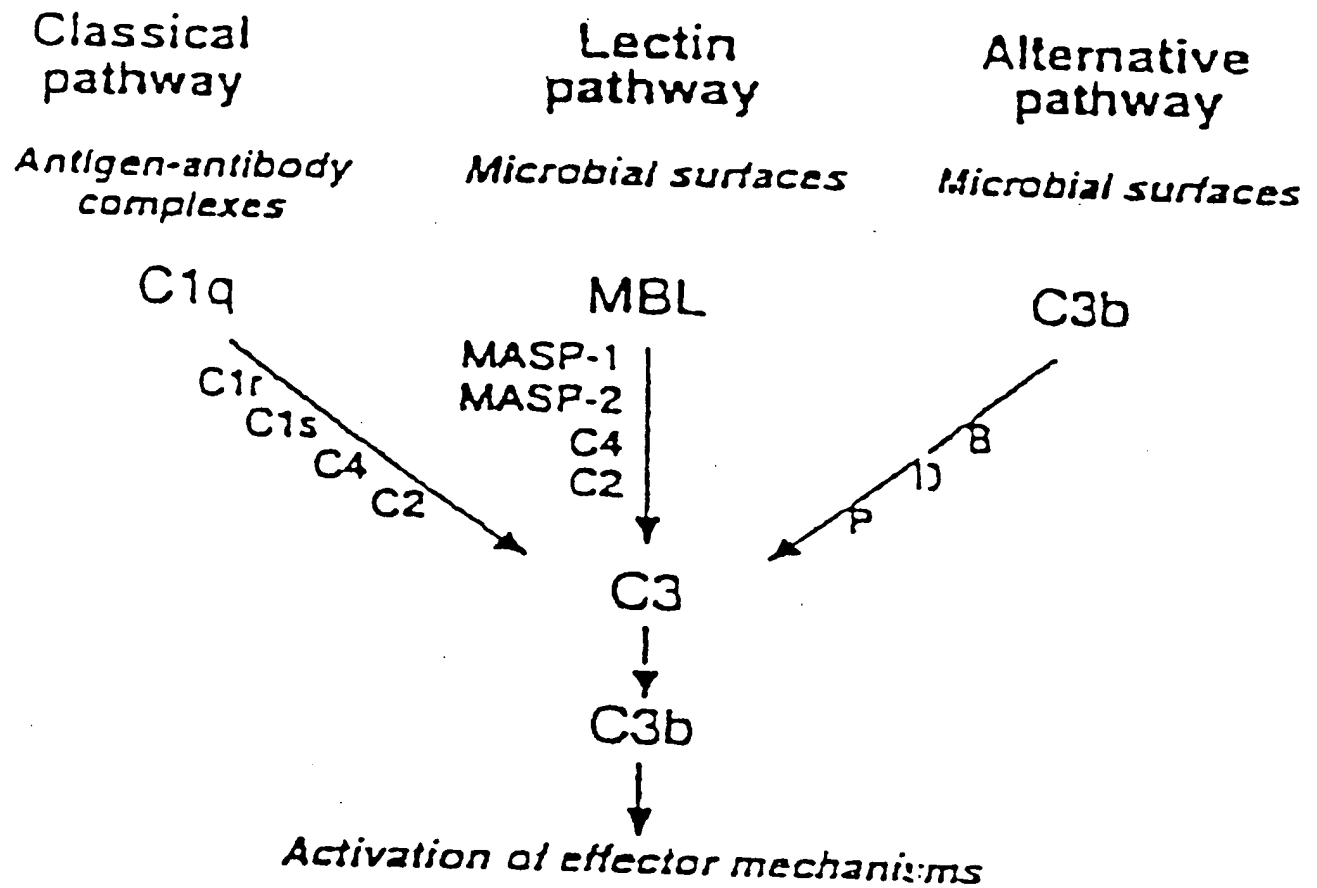


Blot of C1



5/6

Figure 5



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6/6

Figure 6

cctcgtgcacattcggaacagaggctggagcgggcaacaccATGAGCCTGTGCACCTCTCGGGCCTTCTGTGTGCTCGGTGCCCACCCCCTTAGGCCCGAAGT	100
M R G L L T L T C G T L C G S V A T P L C G P K	6
GCCCTGAACCTGTGTTTCGGGCGCCTGGCATCCCCCGGCTTTCACGGGGAGTATGCCAATGACAGGAGCGCGCTCGAACCTGACTGCACCCCCTGGGTATA	200
N P E P V F G R L A S P G F P G E Y A N D Q E R R W T L T A P P G Y	40
C CGCCTGGCCTCTACTTCACCCACTTCGACCTGGAGCTCTCCCACTCTGCGAGTACGACTTCGTCAAG CTGAGCTCGGGGGCCAAAGTGCTGCCACG	300
R L R L Y F T H F D L E L S H L C E Y D F V K L S S G A K V L A T	73
CTGTGCGGCGAGGAGCACAGACAGGAGCGGGCCCTTGGCAAGGCACATTCTTCTACTCGCTGGGCTCS SCCTTGCACATTACCTTCCGCTCCGACTACT	400
L C Q E S T D T E R A P G K D T F Y S L G C S S L D I T F R S D Y	106
CCAACGAGAAGCGGTTTCAACGGGTTTCAGGCGCTTCTATGACGCGAGGACATTCAAGAGTCCAGGTGGGCCCCGGAGAGCGCCCACTCGGACCACCA	500
S N E K P P T G F E A F Y A A E D I D E C Q V J P G E A P T C D H H	140
. CCACACACCTCGGGGCTTCTACTGCTCTGCGCGCGAGGCTACGTCTGTGACCGTAACAGCGGACCTGCTCAGCCCTGTGCTCCGGCCAGGTG	600
C H N H L G G F Y C S C R A G Y V L H R N X R T C S A L C S G Q V	173
TTCACCCAGAGGCTCGGGAGCTCAGCAGCCCTGAATACCCACGCGGTATCCCAAACCTTCCAGTTGCTCTTACAGCATCAGCCTGGAGGAGGGGTTCA	700
F-TQQRSGELSSPEYPRPYPKLSSSCTTYSSIISLEEFGF	206
GTGTCTATTCTCGACTTGTGGAGTCTTCGATGTGGAGACACACCTTCAAAECCTGTGCTCCCTAGGACTTCTCAAGATTCAAAACAGACAGAGAAGAACA	800
S V I L D F V E S F D V E T H P E T T L C P Y D L K I O T D R E E H	240
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G P F C G K T L P H R I E T K S N T V T I T F V T D E S G D H T G	273
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W K I H Y T T C A A Q P C P Y P M A P P H G R V S P V Q A K Y I L K	306
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D S F S I F C E T G Y E L L Q G H L P L K S F I A V C K D G S W D	340
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R P M P A C S I V D C G P P D D L P S G R V E Y I T G P G V T T Y	373
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* AACATGTCATCGGCCCTGGACATTGCAATGGGCCCTGAAAAGACTATCACTCATTATACACUJGCTGTGTGAAGCTGTTTTTATACATGAAG	1600
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D I P I V D H Q K C T A A Y E K P P Y P R G S V T A N H M L C A G L	606
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E S G G K D S C R G D G G A L V F L D S E T E R W F V G G I V S W	640
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G S M N C G E A G Q Y O V Y T K A V I N Y I P # I E N I I S D F stop	671
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gttgtgactctgttaaactcgtctgtccatgctctgtttttaactgtctctctcattgcaaaazaaaaaaaaa	2475

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